

Draft Genome Sequence of a *Halorubrum* H3 Strain Isolated from the Burlinskoye Salt Lake (Altai Krai, Russia)

Aleksey S. Rozanov, Alla V. Bryanskaya, Tatiana K. Malup, Anastasia V. Kotenko, Sergey E. Peltek

Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia

A *Halorubrum* H3 strain was isolated from a water and silt sample from Burlinskoye Lake (Altai Krai, Russia, 53°8'19"N 78°24'27"E). According to 16S rRNA sequences, this strain is most closely related to *Halorubrum saccharovororum*. The completely sequenced and annotated genome is 3,282,373 bp and contains 3,237 genes.

Received 29 April 2015 Accepted 1 May 2015 Published 4 June 2015

Citation Rozanov AS, Bryanskaya AV, Malup TK, Kotenko AV, Peltek SE. 2015. Draft genome sequence of a *Halorubrum* H3 strain isolated from the Burlinskoye salt lake (Altai Krai, Russia). *Genome Announc* 3(3):e00566-15. doi:10.1128/genomeA.00566-15.

Copyright © 2015 Rozanov et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Aleksey S. Rozanov, sibiryak.n@gmail.com

The studied *Halorubrum* H3 strain was isolated from a water and silt sample taken from Burlinskoye (a salt lake in Altai Krai, Russia, 53°8'19"N 78°24'27"E). The water temperature was 20°C at the time of sampling.

The genus *Halorubrum* includes extremely halophilic archaeal species that are widely distributed in high-saline environments and are a major component of the microbial community of hypersaline environments (3 to 5 M) (1). The genus currently contains 26 species. Its representatives are widely distributed in hypersaline environments on almost all continents (2–6).

Halorubrum H3 culture was cultivated in liquid medium containing 1% tryptone, 0.5% yeast extract, and 3.5 M NaCl. Eight milliliters of cell culture was pelleted by centrifugation and resuspended in 75 μ l of H₂O by intense pipetting. DNA was isolated using the DNA purification kit (Fermentas). The Ion PGM Template OT2 400 kit was used to create libraries for genome sequencing. Genome sequencing was performed on an Ion Torrent platform (Applied Biosystems) with Ion 316 chip using the Ion PGM sequencing 400 kit at the Siberian Branch of the Russian Academy of Sciences (SBRAS) Sequencing Center.

De novo assembly of short reads into contigs was performed using SPAdes 3.1.0. Contigs <1,000 bp were deleted. A total of 189 contigs yielded a genome sequence 3,282,373 bp long, with a G+C content of 67.57%. Open reading frame (ORF) prediction and automatic annotation were performed using the NCBI Prokaryotic Genome Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). The complete genome sequence contains 3,237 genes, 2,337 coding sequences (CDSs), 3 rRNAs (5S, 16S, and 23S), 46 tRNAs, and 1 noncoding RNA (ncRNA).

Phylogenetic analysis was performed using 16S rRNA sequences with the unweighted pair group method using average linkages (UPGMA) algorithm implemented in MEGA version 6. The 16S rRNA sequences of *Halorubrum* type strains were found using the StrainInfo (<http://www.straininfo.net>) and GenBank (<http://www.ncbi.nlm.nih.gov/nucleotide>) databases. According

to phylogenetic analysis, the *Halorubrum* H3 strain is most closely related to *Halorubrum saccharovororum*.

Nucleotide sequence accession numbers. The draft genome sequence for *Halorubrum* H3 has been deposited in GenBank under the accession number [JNFB00000000](https://www.ncbi.nlm.nih.gov/nuccore/JNFB00000000). The 189 contigs have been deposited under the accession numbers [JNFB02000001](https://www.ncbi.nlm.nih.gov/nuccore/JNFB02000001) to [JNFB02000189](https://www.ncbi.nlm.nih.gov/nuccore/JNFB02000189).

ACKNOWLEDGMENT

This research was supported by Russia Academy of Science Budget Project VI.58.1.3.

REFERENCES

- McGenity TJ, Grant WD. 1995. Transfer of *Halobacterium saccharovororum*, *Halobacterium sodomense*, *Halobacterium trapanicum* NRC 34021 and *Halobacterium lacusprofundi* to the genus *Halorubrum* gen. nov., as *Halorubrum saccharovororum* comb. nov., *Halorubrum sodomense* comb. nov., *Halorubrum trapanicum* comb. nov., and *Halorubrum lacusprofundi* comb. nov. *Syst Appl Microbiol* 18:237–243. [http://dx.doi.org/10.1016/S0723-2020\(11\)80394-2](http://dx.doi.org/10.1016/S0723-2020(11)80394-2).
- Schneider D, Arp G, Reimer A, Reitner J, Daniel R. 2013. Phylogenetic analysis of a microbialite-forming microbial mat from a hypersaline lake of the Kiritimati Atoll, Central Pacific. *PLoS One* 8:e66662. <http://dx.doi.org/10.1371/journal.pone.0066662>.
- Podell S, Ugalde JA, Narasingarao P, Banfield JF, Heidelberg KB, Allen EE. 2013. Assembly-driven community genomics of a hypersaline microbial ecosystem. *PLoS One* 8:e61692. <http://dx.doi.org/10.1371/journal.pone.0061692>.
- Montoya L, Vizioli C, Rodríguez N, Rastoll MJ, Amils R, Marin I. 2013. Microbial community composition of Tirez Lagoon (Spain), a highly sulfated athalassohaline environment. *Aquat Biosyst* 9:19. <http://dx.doi.org/10.1186/2046-9063-9-19>.
- Bryanskaya AV, Berezhnoy AA, Rozanov AS, Peltek SE, Pavlov AK. 2013. Adaptive capabilities of microorganisms of salt lakes of the Altai region under conditions of early Mars. *Paleontol J* 47:1089–1092. <http://dx.doi.org/10.1134/S0031030113090050>.
- Chen SX, Zhao ZW, Zeng C, Yang ZL. 2013. Phylogenetic analysis of 16S rRNA gene reveals high species diversity of *Halorubrum* in China. *Afr J Microbiol Res* 7:3009–3017.